



Comment

Simple deterministic models and applications
Comment on “Coupled disease–behavior dynamics on complex
networks: A review” by Z. Wang et al.

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Received 25 August 2015; accepted 25 August 2015

Available online 29 August 2015

Communicated by J. Fontanari

Currently, discrete modellings are largely accepted due to the access to computers with huge storage capacity and high performance processors and easy implementation of algorithms, allowing to develop and simulate increasingly sophisticated models. Wang et al. [7] present a review of dynamics in complex networks, focusing on the interaction between disease dynamics and human behavioral and social dynamics. By doing an extensive review regarding to the human behavior responding to disease dynamics, the authors briefly describe the complex dynamics found in the literature: well-mixed populations networks, where spatial structure can be neglected, and other networks considering heterogeneity on spatially distributed populations. As controlling mechanisms are implemented, such as social distancing due ‘social contagion’, quarantine, non-pharmaceutical interventions and vaccination, adaptive behavior can occur in human population, which can be easily taken into account in the dynamics formulated by networked populations.

Complex dynamics encompassing networked populations or dynamics systems with huge number of differential equations (see for instance Marino and Kirschner for tuberculosis [5]) can really capture simultaneously many factors contributing to disease transmission and response of humans to avoid infection. The results provided by these models are notably shedding lights to better understanding of the contagion processes and the improvement of controlling mechanisms. However, simple models can also be useful to address specific questions, which ‘may provide clearer and more rigorous insights than the output of simulation models’ [7]. Some applications of simple deterministic models are described.

Ordinary differential equations can in general be derived as an average behavior of corresponding stochastic process [1]. By defining a random variable regarding to distribution of worms in humans (definitive host), stochastic equations were obtained assuming Markov process [8]. By fitting the prevalence of schistosomiasis data, model parameters were estimated, showing that the assumption of acquired immunity successfully explained the prevalence curve in different regions of the world (Brazil and Tanzania) [9]. By adding another random variable regarding to snail population (intermediate host), and calculating the expectation of random variables, the behavior of worm and snail populations were assessed. The incorporation of acquired immunity in the modelling resulted in a strong robustness of transmission and negative binomial distribution of parasites among humans, showing that the eradication of schistosomiasis could be achieved by treating serologically positive persons, rather than persons with positive stool examination for schistosome eggs [10].

DOI of original article: <http://dx.doi.org/10.1016/j.plrev.2015.07.006>.

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Social behavior can be incorporated in simple modellings. Firstly, an age-structured contact rate can be taken into account [13]. Fitting rubella seroprevalence data from Caieiras City, Brazil, the age-structured contact rate was estimated [12], which agrees in some extent with Fig. 9 shown in [7]. Further, age-dependent force of infection was retrieved, and the paradigm of the delay in the average age of the first infection with vaccination was confronted: this is true in vaccination of elder children, while for vaccination of lower aged children, the average age of the first infection is anticipated [12]. Another social behavior that could be assessed is the effect of educational campaign against HIV infection. Yang and Ferreira [11] assessed how the intensity of the education campaign to avoid HIV infection affects the behavior of the community, and also concluded that the sexual education is better than treatment to reduce HIV infection. Returning to the schistosomiasis, model incorporating age-dependent contact of persons with infested water as describing social behavior can explain the prevalence curve, but not the robustness of schistosome transmission [14].

Deterministic and discrete modellings could complement each other. For instance, to control dengue virus transmission, different types of controls are applied, such as the release of sterilized insects [2]. However, due to the random distribution of breeding sites of mosquito *Aedes aegypti*, this technique should not be suitable. This conclusion cannot be obtained from deterministic model, but discrete model (cellular automata formalism) achieved this goal [3]. Finally, with respect to the dengue spread out, partial differential equations can be used to quantify the velocity of biological invasion [6]. Maidana and Yang [4] estimated the velocity of mosquito *A. aegypti* invasion in the São Paulo State, Brazil, and determined the velocity of dengue propagation depending on temperature.

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